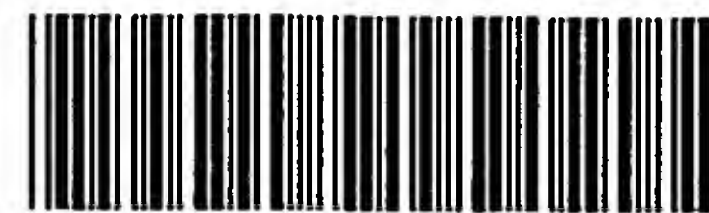


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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,025
Source: IFWP
Date Processed by STIC: 05/23/2006

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PATENT APPLICATION: US/10/579,025

DATE: 05/23/2006

TIME: 14:04:50

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Output Set: N:\CRF4\05232006\J579025.raw

3 <110> APPLICANT: THERION BIOLOGICS CORPORATION
 5 <120> TITLE OF INVENTION: CUSTOM VECTORS FOR TREATING AND PREVENTING PANCREATIC
 6 CANCER
 8 <130> FILE REFERENCE: 700953-53671-PCT
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,025
 C--> 11 <141> CURRENT FILING DATE: 2006-05-11
 13 <150> PRIOR APPLICATION NUMBER: 60/519,354
 14 <151> PRIOR FILING DATE: 2003-11-12
 16 <160> NUMBER OF SEQ ID NOS: 6
 18 <170> SOFTWARE: PatentIn Ver. 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1548
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1
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 28 cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac aagctccgta 180
 29 ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
 30 gccccggcca cggaaccagc ttcaggttca gctgccttgt ggggacagga tgtcacctcg 300
 31 gtaccagtta ctagaccagc tttaggtagc acagcacctc ctgctcatgg agtaactagt 360
 32 gctcctgata ctctccagc tcctggcagt actgcaccac cggcacatgg cgtaacatca 420
 33 gcacctgata caagacctgc acctggatct acagcgccgc ctgcgcacgg agtgacatcg 480
 34 gcgcccagata cgcgccccgc tcccggtagc accgcaccgc ccgcccacgg tgttacaagt 540
 35 gcacccgata cccggccggc acccggaagt accgctccac ctgcacacgg ggtcacaagc 600
 36 gcgcccagaca ctcgacctgc gccagggctg actgcccctc cggcgcacatg tgtgacctca 660
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 38 gctaccacaa ccccagccag caagagcact ccatttctca tcccagcca ccaactctgat 780
 39 actcctacca cccttgccag ccatagcacc aagactgatg ccagtagcac tcaccatagc 840
 40 acggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactgggggtc 900
 41 tctttctttt tcctgtcttt tcacatttca aacctccagt ttaattcctc tctggaagat 960
 42 cccagcaccg actactacca agagctgcag agagacattt ctgaaatgtt tttgcagatt 1020
 43 tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 1080
 44 gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1140
 45 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1200
 46 gtgagtgatg tgccatttcc tttctctgcc cagtctgggg ctgggggtgcc aggctggggc 1260
 47 atcgcgctgc tgggtgctgg ctgtgttctg gttgcgctgg ccattgtcta tctcattgcc 1320
 48 ttggctgtct gtcagtgccg ccgaaagaac tacgggcagc tggacatctt tccagcccgg 1380
 49 gataacctacc atcctatgag cgagtacccc acctaccaca cccatgggag ctatgtgccc 1440
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 51 ctctcttaca caaaccagc agtggcagcc acttctgcca acttgtag 1548
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 515

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56 <212> TYPE: PRT

57 <213> ORGANISM: Homo sapiens

59 <400> SEQUENCE: 2

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60 Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
61   1           5           10           15
63 Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
64           20           25           30
66 Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
67           35           40           45
69 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
70           50           55           60
72 Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
73  65           70           75           80
75 Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Leu Trp Gly Gln
76           85           90           95
78 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Ala
79           100          105          110
81 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
82           115          120          125
84 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Glu Thr
85           130          135          140
87 Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
88 145           150          155          160
90 Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His
91           165          170          175
93 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
94           180          185          190
96 Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro
97           195          200          205
99 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
100          210          215          220
102 Arg Pro Ala Pro Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
103 225          230          235          240
105 Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
106          245          250          255
108 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
109          260          265          270
111 Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
112          275          280          285
114 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
115          290          295          300
117 Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
118 305          310          315          320
120 Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
121          325          330          335
123 Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
124          340          345          350
126 Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
127          355          360          365

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129 Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
130      370                      375                      380
132 Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
133 385                      390                      395                      400
135 Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val
136      405                      410                      415
138 Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala
139      420                      425                      430
141 Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg
142      435                      440                      445
144 Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His
145      450                      455                      460
147 Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro
148 465                      470                      475                      480
150 Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn
151      485                      490                      495
153 Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser
154      500                      505                      510
156 Ala Asn Leu
157      515

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160 <210> SEQ ID NO: 3

161 <211> LENGTH: 2106

162 <212> TYPE: DNA

163 <213> ORGANISM: Homo sapiens

165 <400> SEQUENCE: 3

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166 atggagtctc cctcggtccc tccccacaga tgggtgcatcc cctggcagag gctcctgctc 60
167 acagcctcac ttctaacctt ctggaacccg cccaccactg ccaagctcac tattgaatcc 120
168 acgccgttca atgtcgcaga ggggaaggag gtgcttctac ttgtccacaa tctgccccag 180
169 catctttttg gctacagctg gtacaaaggt gaaagagtgg atggcaaccg tcaaattata 240
170 ggatatgtaa taggaactca acaagctacc ccagggtccc catacagtgg tcgagagata 300
171 atatacccca atgcatccct gctgatccag aacatcatcc agaatgacac aggattctac 360
172 accctacacg tcataaagtc agatcttgtg aatgaagaag caactggcca gttccgggta 420
173 tacccggaac tccctaagcc ttctattagc tccaataata gtaagcctgt cgaagacaaa 480
174 gatgccgtcg cttttacatg cgagcccga aactcaagac caacatatct ctgggtgggtg 540
175 aacaaccagt ccctgcctgt gtcccctaga ctccaactca gcaacggaaa tagaactctg 600
176 accctgttta acgtgaccag gaacgacaca gcaagctaca aatgcgaaac ccaaaatcca 660
177 gtcagcgcca ggaggtctga ttcagtgatt ctcaacgtgc tttacggacc cgatgctcct 720
178 acaatcagcc ctctaaacac aagctataga tcaggggaaa atctgaatct gagctgtcat 780
179 gccgctagca atcctccgc ccaatacagc tggtttgtca atggcacttt ccaacagtcc 840
180 acccaggaac tggttcattcc caatattacc gtgaacaata gtggatccta cacgtgccaa 900
181 gtcacaata gcgacaccgg actcaaccgc acaaccgtga cgacgattac cgtgtatgag 960
182 ccacaaaac cattcataac tagtaacaat tctaaccag ttgaggatga ggacgcagtt 1020
183 gcattaactt gtgagccaga gattcaaat accacttatt tatgggtgggt caataaccaa 1080
184 agtttgccgg ttagcccacg cttgcagttg tctaatagata accgcacatt gacactcctg 1140
185 tccgttactc gcaatgatgt aggaccttat gagggtggca ttcagaatga attatccgtt 1200
186 gatcactccg accctgttat ccttaatgtt ttgtatggcc cagacgaccc aactatatct 1260
187 ccatcataca cctactaccg tcccggcgtg aacttgagcc tttcttgcca tgcagcatcc 1320
188 aacccccctg cacagtactc ctggctgatt gatggaaaca ttcagcagca tactcaagag 1380
189 ttatttataa gcaacataac tgagaagaac agcggactct atacttgcca ggccaataac 1440

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190 tcagccagtg gtcacagcag gactacagtt aaaacaataa ctgtttccgc ggagctgccc 1500
191 aagccctcca tctccagcaa caactccaaa cccgtggagg acaaggatgc tgtggccttc 1560
192 acctgtgaac ctgaggctca gaacacaacc tacctgtggt gggtaaattg tcagagcctc 1620
193 ccagtcagtc ccaggctgca gctgtccaat ggcaacagga ccctcactct attcaatgtc 1680
194 acaagaaatg acgcaagagc ctatgtatgt ggaatccaga actcagtgag tgcaaaccgc 1740
195 agtgacccag tcaccctgga tgtcctctat gggccggaca ccccatcat ttccccccca 1800
196 gactcgtctt acctttcggg agcggacctc aacctctcct gccactcggc ctctaaccga 1860
197 tccccgcagt attcttggcg tatcaatggg ataccgcagc aacacacaca agttctcttt 1920
198 atcgccaaaa tcacgcaaaa taataacggg acctatgcct gttttgtctc taacttggct 1980
199 actggccgca ataattccat agtcaagagc atcacagtct ctgcatctgg aacttctcct 2040
200 ggtctctcag ctggggccac tgtcggcatc atgattggag tgctggttgg gggtgctctg 2100
201 atatag 2106

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204 <210> SEQ ID NO: 4

205 <211> LENGTH: 371

206 <212> TYPE: PRT

207 <213> ORGANISM: Homo sapiens

209 <400> SEQUENCE: 4

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213 Pro Glu Ile Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser
214           20           25           30
216 Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu
217           35           40           45
219 Thr Leu Leu Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly
220           50           55           60
222 Ile Gln Asn Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn
223           65           70           75           80
225 Val Leu Tyr Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr
226           85           90           95
228 Tyr Arg Pro Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn
229           100          105          110
231 Pro Pro Ala Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His
232           115          120          125
234 Thr Gln Glu Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu
235           130          135          140
237 Tyr Thr Cys Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr
238           145          150          155          160
240 Val Lys Thr Ile Thr Val Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser
241           165          170          175
243 Ser Asn Asn Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr
244           180          185          190
246 Cys Glu Pro Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly
247           195          200          205
249 Gln Ser Leu Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg
250           210          215          220
252 Thr Leu Thr Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val
253           225          230          235          240
255 Cys Gly Ile Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr
256           245          250          255

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258 Leu Asp Val Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp
259           260           265           270
261 Ser Ser Tyr Leu Ser Gly Ala Asp Leu Asn Leu Ser Cys His Ser Ala
262           275           280           285
264 Ser Asn Pro Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln
265           290           295           300
267 Gln His Thr Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Gly
268 305           310           315           320
270 Thr Tyr Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser
271           325           330           335
273 Ile Val Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu
274           340           345           350
276 Ser Ala Gly Ala Thr Val Gly Ile Met Ile Gly Val Leu Val Gly Val
277           355           360           365
279 Ala Leu Ile
280           370
283 <210> SEQ ID NO: 5
284 <211> LENGTH: 31
285 <212> TYPE: DNA
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
290     primer
292 <400> SEQUENCE: 5
293 ggtaccggta ccatggaagg ggaaggggtt c                               31
296 <210> SEQ ID NO: 6
297 <211> LENGTH: 31
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial Sequence
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
303     primer
305 <400> SEQUENCE: 6
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VERIFICATION SUMMARY

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